CRF Errors Corrected by the STIC Systems Branch

01P12

Serial Number: 09/267,963

CRF Processing Date: 3/30/99
Edited by: _____
Verified by: _____ (STIC staff)

☐ Changed a file from non-ASCII to ASCII

☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.

☐ Edited a format error in the Current Application Data section, specifically: _____

ENTERED

☑ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____.

☐ Added the mandatory heading and subheadings for "Current Application Data".

☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically:

_____

☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:

_____

☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

_____

☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

☐ Inserted colons after headings/subheadings. Headings edited included:

_____

☐ Deleted extra, invalid, headings used by an applicant, specifically:

_____

☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____.

☐ Inserted mandatory headings, specifically: _____

☐ Corrected an obvious error in the response, specifically:

_____

☐ Edited identifiers where upper case is used but lower case is required, or vice versa.

☐ Corrected an error in the Number of Sequences field, specifically:

_____

☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

☐ Deleted ***ending*** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____

☐ Other:

_____

_____

_____

_____

***Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.**

3/1/95

This Raw Listing contains the General Information Section and up to the first 5 pages.

Does Not Comply
Corrected Diskette Needed

SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: Kohei MIYAZONO, Takeshe IMAMURA, Peter ten

(ii) TITLE OF INVENTION: ISOLATED ALK-1 PROTEIN, ENCODING IT, AND USES THEREOF

(iii) NUMBER OF SEQUENCES: 29

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Fulbright & Jaworski L.
(B) STREET: 666 Fifth Avenue
(C) CITY: New York City
(D) STATE: New York
(E) COUNTRY: USA
(F) ZIP: 10103

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette, 3.25 inch, 1.44mb
(B) COMPUTER: IBM PS/2
(C) OPERATING SYSTEM: PC-DOS
(D) SOFTWARE: Wordperfect

(vi) CURRENT APPLICATION DATA:
--> **(A) APPLICATION NUMBER: 09/039,177**
(B) FILING DATE: March 13, 1998
--> **(C) CLASSIFICATION: 435**

(vii)PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: PCT/GB93/0236
(B) FILING DATE: November 17, 1993

(vii)PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: GB 9224057.1
(B) FILING DATE: November 17, 1992

(vii)PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: GB 9304677.9
(B) FILING DATE: March 8, 1993

(vii)PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: GB 9304680.3
(B) FILING DATE: March 8, 1993

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47        (vii)PRIOR APPLICATION DATA:
48             (A) APPLICATION NUMBER: 9311047.6
49             (B) FILING DATE: May 28, 1993
50
51        (vii)PRIOR APPLICATION DATA:
52             (A) APPLICATION NUMBER: 9313763.6
53             (B) FILING DATE: July 2, 1993
54
55
56        (vii)PRIOR APPLICATION DATA:
57             (A) APPLICATION NUMBER: 9136099.2
58             (B) FILING DATE: August 3, 1993
59
60        (vii)PRIOR APPLICATION DATA:
61             (A) APPLICATION NUMBER: 321344.5
62             (B) FILING DATE: October 15, 1993
63
64        (viii)ATTORNEY/AGENT INFORMATION:
65             (A) NAME: Mary Anne Schofield
66             (B) REGISTRATION NUMBER: 36,669
67             (C) REFERENCE/DOCKET NUMBER: LUD 5539.1 CIP - JEL/MAS
68
69        (ix) TELECOMMUNICATION INFORMATION:
70                                    (A) TELEPHONE: (212) 318-3000
71                                    (B) TELEFAX:   (212) 752-5958
72
73
74
75    (2) INFORMATION FOR SEQ ID NO: 1:
76
77        (i) SEQUENCE CHARACTERISTICS:
78             (A) LENGTH: 1984 base pairs
79             (B) TYPE: nucleic acid
80             (C) STRANDEDNESS: unknown
81             (D) TOPOLOGY: linear
82
83       (ii) MOLECULE TYPE: cDNA
84
85      (iii) HYPOTHETICAL: NO
86
87      (iii) ANTI-SENSE: NO
88
89        (v) FRAGMENT TYPE: internal
90
91       (vi) ORIGINAL SOURCE:
92             (A) ORGANISM: Homo sapiens
93
94       (ix) FEATURE:
95             (A) NAME/KEY: CDS
96             (B) LOCATION: 283..1791
97
98       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
99
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```
100  AGGAAACGGT TTATTAGGAG GGAGTGGTGG AGCTGGGCCA GGCAGGAAGA CGCTGGAATA      60
101
102  AGAAACATTT TTGCTCCAGC CCCCATCCCA GTCCCGGGAG GCTGCCGCGC CAGCTGCGCC     120
103
104  GAGCGAGCCC CTCCCCGGCT CCAGCCCGGT CCGGGGCCGC GCCGGACCCC AGCCCGCCGT     180
105
106  CCAGCGCTGG CGGTGCAACT GCGGCCGCGC GGTGGAGGGG AGGTGGCCCC GGTCCGCCGA     240
107
108  AGGCTAGCGC CCCGCCACCC GCAGAGCGGG CCCAGAGGGA CC ATG ACC TTG GGC         294
109                                                   Met Thr Leu Gly
110                                                     1
111
112  TCC CCC AGG AAA GGC CTT CTG ATG CTG CTG ATG GCC TTG GTG ACC CAG        342
113  Ser Pro Arg Lys Gly Leu Leu Met Leu Leu Met Ala Leu Val Thr Gln
114    5                  10                  15                  20
115
116  GGA GAC CCT GTG AAG CCG TCT CGG GGC CCG CTG GTG ACC TGC ACG TGT        390
117  Gly Asp Pro Val Lys Pro Ser Arg Gly Pro Leu Val Thr Cys Thr Cys
118                  25                  30                  35
119
120  GAG AGC CCA CAT TGC AAG GGG CCT ACC TGC CGG GGG GCC TGG TGC ACA        438
121  Glu Ser Pro His Cys Lys Gly Pro Thr Cys Arg Gly Ala Trp Cys Thr
122              40                  45                  50
123
124  GTA GTG CTG GTG CGG GAG GAG GGG AGG CAC CCC CAG GAA CAT CGG GGC        486
125  Val Val Leu Val Arg Glu Glu Gly Arg His Pro Gln Glu His Arg Gly
126           55                  60                  65
127
128  TGC GGG AAC TTG CAC AGG GAG CTC TGC AGG GGG CGC CCC ACC GAG TTC        534
129  Cys Gly Asn Leu His Arg Glu Leu Cys Arg Gly Arg Pro Thr Glu Phe
130       70                  75                  80
131
132  GTC AAC CAC TAC TGC TGC GAC AGC CAC CTC TGC AAC CAC AAC GTG TCC        582
133  Val Asn His Tyr Cys Cys Asp Ser His Leu Cys Asn His Asn Val Ser
134   85                  90                  95                 100
135
136  CTG GTG CTG GAG GCC ACC CAA CCT CCT TCG GAG CAG CCG GGA ACA GAT        630
137  Leu Val Leu Glu Ala Thr Gln Pro Pro Ser Glu Gln Pro Gly Thr Asp
138                 105                 110                 115
139
140  GGC CAG CTG GCC CTG ATC CTG GGC CCC GTG CTG GCC TTG CTG GCC CTG        678
141  Gly Gln Leu Ala Leu Ile Leu Gly Pro Val Leu Ala Leu Leu Ala Leu
142              120                 125                 130
143
144  GTG GCC CTG GGT GTC CTG GGC CTG TGG CAT GTC CGA CGG AGG CAG GAG        726
145  Val Ala Leu Gly Val Leu Gly Leu Trp His Val Arg Arg Arg Gln Glu
146           135                 140                 145
147
148  AAG CAG CGT GGC CTG CAC AGC GAG CTG GGA GAG TCC AGT CTC ATC CTG        774
149  Lys Gln Arg Gly Leu His Ser Glu Leu Gly Glu Ser Ser Leu Ile Leu
150       150                 155                 160
151
152  AAA GCA TCT GAG CAG GGC GAC ACG ATG TTG GGG GAC CTC CTG GAC AGT        822
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Lys Ala Ser Glu Gln Gly Asp Thr Met Leu Gly Asp Leu Leu Asp Ser
165                 170                 175                 180

GAC TGC ACC ACA GGG AGT GGC TCA GGG CTC CCC TTC CTG GTG CAG AGG       870
Asp Cys Thr Thr Gly Ser Gly Ser Gly Leu Pro Phe Leu Val Gln Arg
                185                 190                 195

ACA GTG GCA CGG CAG GTT GCC TTG GTG GAG TGT GTG GGA AAA GGC CGC       918
Thr Val Ala Arg Gln Val Ala Leu Val Glu Cys Val Gly Lys Gly Arg
            200                 205                 210

TAT GGC GAA GTG TGG CGG GGC TTG TGG CAC GGT GAG AGT GTG GCC GTC       966
Tyr Gly Glu Val Trp Arg Gly Leu Trp His Gly Glu Ser Val Ala Val
        215                 220                 225

AAG ATC TTC TCC TCG AGG GAT GAA CAG TCC TGG TTC CGG GAG ACT GAG      1014
Lys Ile Phe Ser Ser Arg Asp Glu Gln Ser Trp Phe Arg Glu Thr Glu
    230                 235                 240

ATC TAT AAC ACA GTA TTG CTC AGA CAC GAC AAC ATC CTA GGC TTC ATC      1062
Ile Tyr Asn Thr Val Leu Leu Arg His Asp Asn Ile Leu Gly Phe Ile
245                 250                 255                 260

GCC TCA GAC ATG ACC TCC CGC AAC TCG AGC ACG CAG CTG TGG CTC ATC      1110
Ala Ser Asp Met Thr Ser Arg Asn Ser Ser Thr Gln Leu Trp Leu Ile
                265                 270                 275

ACG CAC TAC CAC GAG CAC GGC TCC CTC TAC GAC TTT CTG CAG AGA CAG      1158
Thr His Tyr His Glu His Gly Ser Leu Tyr Asp Phe Leu Gln Arg Gln
            280                 285                 290

ACG CTG GAG CCC CAT CTG GCT CTG AGG CTA GCT GTG TCC GCG GCA TGC      1206
Thr Leu Glu Pro His Leu Ala Leu Arg Leu Ala Val Ser Ala Ala Cys
        295                 300                 305

GGC CTG GCG CAC CTG CAC GTG GAG ATC TTC GGT ACA CAG GGC AAA CCA      1254
Gly Leu Ala His Leu His Val Glu Ile Phe Gly Thr Gln Gly Lys Pro
    310                 315                 320

GCC ATT GCC CAC CGC GAC TTC AAG AGC CGC AAT GTG CTG GTC AAG AGC      1302
Ala Ile Ala His Arg Asp Phe Lys Ser Arg Asn Val Leu Val Lys Ser
325                 330                 335                 340

AAC CTG CAG TGT TGC ATC GCC GAC CTG GGC CTG GCT GTG ATG CAC TCA      1350
Asn Leu Gln Cys Cys Ile Ala Asp Leu Gly Leu Ala Val Met His Ser
                345                 350                 355

CAG GGC AGC GAT TAC CTG GAC ATC GGC AAC AAC CCG AGA GTG GGC ACC      1398
Gln Gly Ser Asp Tyr Leu Asp Ile Gly Asn Asn Pro Arg Val Gly Thr
            360                 365                 370

AAG CGG TAC ATG GCA CCC GAG GTG CTG GAC GAG CAG ATC CGC ACG GAC      1446
Lys Arg Tyr Met Ala Pro Glu Val Leu Asp Glu Gln Ile Arg Thr Asp
```

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206          375                 380                 385
207
208  TGC TTT GAG TCC TAC AAG TGG ACT GAC ATC TGG GCC TTT GGC CTG GTG      1494
209  Cys Phe Glu Ser Tyr Lys Trp Thr Asp Ile Trp Ala Phe Gly Leu Val
210      390                 395                 400
211
212  CTG TGG GAG ATT GCC CGC CGG ACC ATC GTG AAT GGC ATC GTG GAG GAC      1542
213  Leu Trp Glu Ile Ala Arg Arg Thr Ile Val Asn Gly Ile Val Glu Asp
214  405                 410                 415                 420
215
216  TAT AGA CCA CCC TTC TAT GAT GTG GTG CCC AAT GAC CCC AGC TTT GAG      1590
217  Tyr Arg Pro Pro Phe Tyr Asp Val Val Pro Asn Asp Pro Ser Phe Glu
218                  425                 430                 435
219
220  GAC ATG AAG AAG GTG GTG TGT GTG GAT CAG CAG ACC CCC ACC ATC CCT      1638
221  Asp Met Lys Lys Val Val Cys Val Asp Gln Gln Thr Pro Thr Ile Pro
222              440                 445                 450
223
224  AAC CGG CTG GCT GCA GAC CCG GTC CTC TCA GGC CTA GCT CAG ATG ATG      1686
225  Asn Arg Leu Ala Ala Asp Pro Val Leu Ser Gly Leu Ala Gln Met Met
226          455                 460                 465
227
228  CGG GAG TGC TGG TAC CCA AAC CCC TCT GCC CGA CTC ACC GCG CTG CGG      1734
229  Arg Glu Cys Trp Tyr Pro Asn Pro Ser Ala Arg Leu Thr Ala Leu Arg
230      470                 475                 480
231
232  ATC AAG AAG ACA CTA CAA AAA ATT AGC AAC AGT CCA GAG AAG CCT AAA      1782
233  Ile Lys Lys Thr Leu Gln Lys Ile Ser Asn Ser Pro Glu Lys Pro Lys
234  485                 490                 495                 500
235
236  GTG ATT CAA TAGCCCAGGA GCACCTGATT CCTTTCTGCC TGCAGGGGGC              1831
237  Val Ile Gln
238
239  TGGGGGGGTG GGGGGCAGTG GATGGTGCCC TATCTGGGTA GAGGTAGTGT GAGTGTGGTG    1891
240
241  TGTGCTGGGG ATGGGCAGCT GCGCCTGCCT GCTCGGCCCC CAGCCCACCC AGCCAAAAAT    1951
242
243  ACAGCTGGGC TGAAACCTGA AAAAAAAAAA AAA                                  1984
244
245
246  (2) INFORMATION FOR SEQ ID NO: 2:
247
248         (i) SEQUENCE CHARACTERISTICS:
249            (A) LENGTH: 503 amino acids
250            (B) TYPE: amino acid
251            (D) TOPOLOGY: linear
252
253      (ii) MOLECULE TYPE: protein
254
255      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
256
257  Met Thr Leu Gly Ser Pro Arg Lys Gly Leu Leu Met Leu Leu Met Ala
258    1               5                  10                  15
```

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/09/267,963*

DATE: 03/30/1999
TIME: 08:51:22

INPUT SET: S31256.raw

Line	Error	Original Text
27	Wrong application Serial Number	(A) APPLICATION NUMBER: 09/039,177
29	Wrong Classification	(C) CLASSIFICATION: 435